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#3

SEQUENCE LISTING

<110> Reindl, Andreas
Mejia, Patricia Leon
Palmas, Juan Manual Esteves
Gracia, Maria Araceli Cantero
Ebneeth, Marcus
Herbers, Karin

<120> DNA sequence coding for a 1-deoxy-D-xylulose-5-phosphate synthase and overproduction thereof in plants

<130> 0817/000006/MEC

<140> US 09/762,045
<141> 2001-02-01

<150> PCT/EP99/05467
<151> 1999-07-30

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<170> PatentIn Vers. 2.0/WordPerfect 6.0

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			20					25					30			
Asp	Glu	Leu	Arg	Arg	Tyr	Leu	Leu	Asp	Ser	Val	Ser	Arg	Ser	Ser	Gly	
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His	Phe	Ala	Ser	Gly	Leu	Gly	Thr	Val	Glu	Leu	Thr	Val	Ala	Leu	His	
	50					55					60					
Tyr	Val	Tyr	Asn	Thr	Pro	Phe	Asp	Gln	Leu	Ile	Trp	Asp	Val	Gly	His	
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Gln	Ala	Tyr	Pro	His	Lys	Ile	Leu	Thr	Gly	Arg	Arg	Asp	Lys	Ile	Gly	
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Ser	Glu	Tyr	Asp	Val	Leu	Ser	Val	Gly	His	Ser	Ser	Thr	Ser	Ile	Ser	
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				165					170					175		
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Asn	Asn	His	Leu	Ala	Gln	Leu	Leu	Ser	Gly	Lys	Leu	Tyr	Ser	Ser	Leu	
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Arg	Glu	Gly	Gly	Lys	Lys	Val	Phe	Ser	Gly	Val	Pro	Pro	Ile	Lys	Glu	
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Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly
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 Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly
 245 250 255
 His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu
 260 265 270
 Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr
 275 280 285
 Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe
 290 295 300
 Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser
 305 310 315 320
 Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp
 325 330 335
 Asn Lys Leu Met Ala Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Met
 340 345 350
 Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile
 355 360 365
 Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly
 370 375 380
 Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr
 385 390 395 400
 Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe
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 Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln
 420 425 430
 Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile
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 Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly
 450 455 460
 Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn
 465 470 475 480
 Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys
 485 490 495
 Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly
 500 505 510
 Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr
 515 520 525
 Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu

530	535	540
Glu Met Ala Ala Ser His 545	Glu Ala Leu Val Thr 550	Val Glu Glu Asn Ala 555 560
Ile Met Gly Gly Ala Gly Ser Gly Val 565	Asn Glu Val Leu Met Ala His 570 575	
Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile 580 585 590		
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 <222> (218)..(1138)

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gagcactccg atgcgcggct cccgcgccag cagcaccagg agccggccgt ccagatgatc 180
gatcgccacg gcagcccctc cagtgggtcat cctgtac atg cag ccc cac gcc atg 235
                               Met Gln Pro His Ala Met
                               1           5

ggc ggt gca ctg aac aca ttg tcc agc gga caa gcc aac tat tgc gca 283
Gly Gly Ala Leu Asn Thr Leu Ser Ser Gly Gln Ala Asn Tyr Cys Ala
                10                15                20

cct tgc gga acg gag cga ccc tgc cgc cat gac gca gac cac aca cca 331
Pro Cys Gly Thr Glu Arg Pro Cys Arg His Asp Ala Asp His Thr Pro
                25                30                35

cac tcc cga cac cgc ccg gca ggc cga ccc ctt ccc ggt gaa ggg aat 379
His Ser Arg His Arg Pro Ala Gly Arg Pro Leu Pro Gly Glu Gly Asn
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gga cgc ggt cgt ctt cgc cgt agg caa cgc caa gca ggc cgc gca cta 427
Gly Arg Gly Arg Leu Arg Arg Arg Gln Arg Gln Ala Gly Arg Ala Leu
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ctc cac cgc ctt cgg cat gca gct tgt ggc gta ctc cgg acc gga gaa 475
Leu His Arg Leu Arg His Ala Ala Cys Gly Val Leu Arg Thr Gly Glu
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cgg cag ccg cga gac cgc ttc gta cgt cct cac caa cgg ctc ggc acg	523
Arg Gln Pro Arg Asp Arg Phe Val Arg Pro His Gln Arg Leu Gly Thr	
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ctt cgt cct cac ctc cgt cat caa gcc cgc cac ccc ctg ggg cca ctt	571
Leu Arg Pro His Leu Arg His Gln Ala Arg His Pro Leu Gly Pro Leu	
105 110 115	
cct cgc cga cca tgt ggc cga gca cgg cga cgg cgt cgt cga cct cgc	619
Pro Arg Arg Pro Cys Gly Arg Ala Arg Arg Arg Arg Arg Arg Pro Arg	
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cat cga ggt ccc gga cgc ccg cgc cgc cca cgc gta cgc gat cga gca	667
His Arg Gly Pro Gly Arg Pro Arg Arg Pro Arg Val Arg Asp Arg Ala	
135 140 145 150	
cgg cgc ccg ctc ggt cgc cga gcc gta cga gct gaa gga cga gca cgg	715
Arg Arg Pro Leu Gly Arg Arg Ala Val Arg Ala Glu Gly Arg Ala Arg	
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cac ggt cgt cct cgc cgc gat cgc cac cta cgg caa gac ccg cca cac	763
His Gly Arg Pro Arg Arg Asp Arg His Leu Arg Gln Asp Pro Pro His	
170 175 180	
cct cgt cga ccg gac cgg cta cga cgg ccc cta cct ccc cgg cta cgt	811
Pro Arg Arg Pro Asp Arg Leu Arg Arg Pro Leu Pro Pro Arg Leu Arg	
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Gly Arg Arg Pro Asp Arg Arg Thr Ala Arg Pro Pro His Leu Pro Gly	
200 205 210	
cat cga cca ctg cgt cgg caa cgt cga gct cgg ccg gat gaa cga atg	907
His Arg Pro Leu Arg Arg Gln Arg Arg Ala Arg Pro Asp Glu Arg Met	
215 220 225 230	
ggt cgg ctt cta caa caa ggt cat ggg ctt cac gaa cat gaa gga gtt	955
Gly Arg Leu Leu Gln Gln Gly His Gly Leu His Glu His Glu Gly Val	
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Arg Gly Arg Arg His Arg Asp Arg Val Leu Gly Ala Asp Val Glu Gly	
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Arg Gly Arg Arg His Ala Gln Gly Gln Val Pro Asp Gln Arg Ala Arg	
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Pro Arg Gln Glu Glu Val Pro Asp Arg Arg Val Pro Gly Val Leu Arg	
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Arg Arg Gly Arg Pro Ala His Arg Ala Glu His Gly	
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gacaccctcg gggagtgggt gggcgacacc cgcgtccccg tcgacaccct gcgcgagctg	1268

aagatcctcg cggaccgcga cgaggacggc tatctgctcc agatcttcac caagccggtc 1328
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Asp	Ala	Asp	His	Thr	Pro	His	Ser	Arg	His	Arg	Pro	Ala	Gly	Arg	Pro	35	40	45	
Leu	Pro	Gly	Glu	Gly	Asn	Gly	Arg	Gly	Arg	Leu	Arg	Arg	Arg	Gln	Arg	50	55	60	
Gln	Ala	Gly	Arg	Ala	Leu	Leu	His	Arg	Leu	Arg	His	Ala	Ala	Cys	Gly	65	70	75	80
Val	Leu	Arg	Thr	Gly	Glu	Arg	Gln	Pro	Arg	Asp	Arg	Phe	Val	Arg	Pro	85	90	95	
His	Gln	Arg	Leu	Gly	Thr	Leu	Arg	Pro	His	Leu	Arg	His	Gln	Ala	Arg	100	105	110	
His	Pro	Leu	Gly	Pro	Leu	Pro	Arg	Arg	Pro	Cys	Gly	Arg	Ala	Arg	Arg	115	120	125	
Arg	Arg	Arg	Arg	Pro	Arg	His	Arg	Gly	Pro	Gly	Arg	Pro	Arg	Arg	Pro	130	135	140	
Arg	Val	Arg	Asp	Arg	Ala	Arg	Arg	Pro	Leu	Gly	Arg	Arg	Ala	Val	Arg	145	150	155	160
Ala	Glu	Gly	Arg	Ala	Arg	His	Gly	Arg	Pro	Arg	Arg	Asp	Arg	His	Leu	165	170	175	
Arg	Gln	Asp	Pro	Pro	His	Pro	Arg	Arg	Pro	Asp	Arg	Leu	Arg	Arg	Pro	180	185	190	
Leu	Pro	Pro	Arg	Leu	Arg	Gly	Arg	Arg	Pro	Asp	Arg	Arg	Thr	Ala	Arg	195	200	205	
Pro	Pro	His	Leu	Pro	Gly	His	Arg	Pro	Leu	Arg	Arg	Gln	Arg	Arg	Ala	210	215	220	

Arg Pro Asp Glu Arg Met Gly Arg Leu Leu Gln Gln Gly His Gly Leu
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 His Glu His Glu Gly Val Arg Gly Arg Arg His Arg Asp Arg Val Leu
 245 250 255
 Gly Ala Asp Val Glu Gly Arg Gly Arg Arg His Ala Gln Gly Gln Val
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Ser Thr Glu Gln Thr Asn Phe Val Ser His Val Pro Ser Ser Leu Ser	
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Leu Pro Gln Arg Arg Thr Ser Leu Arg Val Thr Ala Ala Arg Ala Thr	
35 40 45	
ccc aaa ctc tcc aac cgt aaa ctc cgt gtc gcc gtc atc ggt ggt gga	192
Pro Lys Leu Ser Asn Arg Lys Leu Arg Val Ala Val Ile Gly Gly Gly	
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cca gca ggc ggg gca gct gca gag act cta gca caa gga gga atc gag	240
Pro Ala Gly Gly Ala Ala Ala Glu Thr Leu Ala Gln Gly Gly Ile Glu	
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acg att ctc atc gag cgt aag atg gac aat tgc aag cct tgc ggt ggc	288
Thr Ile Leu Ile Glu Arg Lys Met Asp Asn Cys Lys Pro Cys Gly Gly	
85 90 95	
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Ala Ile Pro Leu Cys Met Val Gly Glu Phe Asn Leu Pro Leu Asp Ile	
100 105 110	
att gat cgg aga gtg acg aag atg aag atg att tcg ccg tcg aac att	384

Ile	Asp	Arg	Arg	Val	Thr	Lys	Met	Lys	Met	Ile	Ser	Pro	Ser	Asn	Ile	
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gct	gtt	gat	att	ggc	cgt	acg	ctt	aag	gag	cat	gag	tat	ata	ggc	atg	432
Ala	Val	Asp	Ile	Gly	Arg	Thr	Leu	Lys	Glu	His	Glu	Tyr	Ile	Gly	Met	
	130						135				140					
gtg	aga	aga	gaa	gtt	ctt	gat	gct	tat	ctg	aga	gag	aga	gct	gag	aag	480
Val	Arg	Arg	Glu	Val	Leu	Asp	Ala	Tyr	Leu	Arg	Glu	Arg	Ala	Glu	Lys	
145					150				155						160	
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Ser	Gly	Ala	Thr	Val	Ile	Asn	Gly	Leu	Phe	Leu	Lys	Met	Asp	His	Pro	
				165				170						175		
gag	aat	tgg	gac	tcg	ccg	tac	act	ttg	cat	tac	act	gag	tac	gat	ggc	576
Glu	Asn	Trp	Asp	Ser	Pro	Tyr	Thr	Leu	His	Tyr	Thr	Glu	Tyr	Asp	Gly	
			180					185					190			
aaa	act	gga	gct	aca	ggg	acg	aag	aaa	aca	atg	gag	gtt	gat	gct	gtc	624
Lys	Thr	Gly	Ala	Thr	Gly	Thr	Lys	Lys	Thr	Met	Glu	Val	Asp	Ala	Val	
		195					200					205				
att	gga	gct	gat	gga	gct	aac	tct	agg	gtt	gct	aaa	tct	att	gat	gct	672
Ile	Gly	Ala	Asp	Gly	Ala	Asn	Ser	Arg	Val	Ala	Lys	Ser	Ile	Asp	Ala	
	210					215					220					
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Gly	Asp	Tyr	Asp	Tyr	Ala	Ile	Ala	Phe	Gln	Glu	Arg	Ile	Arg	Ile	Pro	
225					230				235						240	
gat	gag	aaa	atg	act	tac	tat	gag	gat	tta	gct	gag	atg	tat	gtt	gga	768
Asp	Glu	Lys	Met	Thr	Tyr	Tyr	Glu	Asp	Leu	Ala	Glu	Met	Tyr	Val	Gly	
				245					250					255		
gat	gat	gtg	tcg	ccg	gat	ttc	tat	ggc	tgg	gtg	ttc	cct	aag	tgc	gac	816
Asp	Asp	Val	Ser	Pro	Asp	Phe	Tyr	Gly	Trp	Val	Phe	Pro	Lys	Cys	Asp	
		260						265					270			
cat	gta	gct	gtt	gga	aca	ggc	act	gtg	act	cac	aaa	ggc	gac	atc	aag	864
His	Val	Ala	Val	Gly	Thr	Gly	Thr	Val	Thr	His	Lys	Gly	Asp	Ile	Lys	
		275					280					285				
aag	ttc	cag	ctc	gcg	acc	aga	aac	aga	gct	aag	gac	aag	att	ctt	gga	912
Lys	Phe	Gln	Leu	Ala	Thr	Arg	Asn	Arg	Ala	Lys	Asp	Lys	Ile	Leu	Gly	
	290					295					300					
ggg	aag	atc	atc	cgt	gtg	gag	gct	cat	ccg	att	cct	gaa	cat	ccg	aga	960
Gly	Lys	Ile	Ile	Arg	Val	Glu	Ala	His	Pro	Ile	Pro	Glu	His	Pro	Arg	
305					310				315						320	
cca	cgt	agg	ctc	tcg	aaa	cgt	gtg	gct	ctt	gta	ggc	gat	gct	gca	ggg	1008
Pro	Arg	Arg	Leu	Ser	Lys	Arg	Val	Ala	Leu	Val	Gly	Asp	Ala	Ala	Gly	
				325					330					335		
tat	gtg	act	aaa	tgc	tct	ggc	gaa	ggg	atc	tac	ttt	gct	gct	aag	agt	1056
Tyr	Val	Thr	Lys	Cys	Ser	Gly	Glu	Gly	Ile	Tyr	Phe	Ala	Ala	Lys	Ser	
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 Lys Thr Tyr Leu Pro Thr Tyr Arg Val Leu Asp Val Leu Gln Lys Val
 385 390 395 400
 ttt tac aga tca aat ccg gct aga gaa gcg ttt gtg gag atg tgt aat 1248
 Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn
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 gat gag tat gtt cag aag atg aca ttc gat agc tat ctg tac aag cgg 1296
 Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg
 420 425 430
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 Ile Gly Ser Leu Val Arg Ala Asn Ala Leu Arg Arg Glu Ile Glu Lys
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 ctt agt gtt taagaaacaa ataatgaggt ctatctcctt tcttcatctc 1441
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 <213> *Arabidopsis thaliana*

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 Pro Lys Leu Ser Asn Arg Lys Leu Arg Val Ala Val Ile Gly Gly Gly
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 Pro Ala Gly Gly Ala Ala Ala Glu Thr Leu Ala Gln Gly Gly Ile Glu
 65 70 75 80
 Thr Ile Leu Ile Glu Arg Lys Met Asp Asn Cys Lys Pro Cys Gly Gly

85							90							95						
Ala	Ile	Pro	Leu	Cys	Met	Val	Gly	Glu	Phe	Asn	Leu	Pro	Leu	Asp	Ile					
			100				105						110							
Ile	Asp	Arg	Arg	Val	Thr	Lys	Met	Lys	Met	Ile	Ser	Pro	Ser	Asn	Ile					
			115				120						125							
Ala	Val	Asp	Ile	Gly	Arg	Thr	Leu	Lys	Glu	His	Glu	Tyr	Ile	Gly	Met					
			130				135						140							
Val	Arg	Arg	Glu	Val	Leu	Asp	Ala	Tyr	Leu	Arg	Glu	Arg	Ala	Glu	Lys					
			145				150						155							
Ser	Gly	Ala	Thr	Val	Ile	Asn	Gly	Leu	Phe	Leu	Lys	Met	Asp	His	Pro					
			165							170			175							
Glu	Asn	Trp	Asp	Ser	Pro	Tyr	Thr	Leu	His	Tyr	Thr	Glu	Tyr	Asp	Gly					
			180				185						190							
Lys	Thr	Gly	Ala	Thr	Gly	Thr	Lys	Lys	Thr	Met	Glu	Val	Asp	Ala	Val					
			195				200						205							
Ile	Gly	Ala	Asp	Gly	Ala	Asn	Ser	Arg	Val	Ala	Lys	Ser	Ile	Asp	Ala					
			210				215						220							
Gly	Asp	Tyr	Asp	Tyr	Ala	Ile	Ala	Phe	Gln	Glu	Arg	Ile	Arg	Ile	Pro					
			225				230						235							
Asp	Glu	Lys	Met	Thr	Tyr	Tyr	Glu	Asp	Leu	Ala	Glu	Met	Tyr	Val	Gly					
			245				250						255							
Asp	Asp	Val	Ser	Pro	Asp	Phe	Tyr	Gly	Trp	Val	Phe	Pro	Lys	Cys	Asp					
			260				265						270							
His	Val	Ala	Val	Gly	Thr	Gly	Thr	Val	Thr	His	Lys	Gly	Asp	Ile	Lys					
			275				280						285							
Lys	Phe	Gln	Leu	Ala	Thr	Arg	Asn	Arg	Ala	Lys	Asp	Lys	Ile	Leu	Gly					
			290				295						300							
Gly	Lys	Ile	Ile	Arg	Val	Glu	Ala	His	Pro	Ile	Pro	Glu	His	Pro	Arg					
			305				310						315							
Pro	Arg	Arg	Leu	Ser	Lys	Arg	Val	Ala	Leu	Val	Gly	Asp	Ala	Ala	Gly					
			325				330						335							
Tyr	Val	Thr	Lys	Cys	Ser	Gly	Glu	Gly	Ile	Tyr	Phe	Ala	Ala	Lys	Ser					
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Lys	Met	Ile	Asp	Glu	Gly	Asp	Leu	Arg	Lys	Tyr	Leu	Glu	Lys	Trp	Asp					
			370				375						380							
Lys	Thr	Tyr	Leu	Pro	Thr	Tyr	Arg	Val	Leu	Asp	Val	Leu	Gln	Lys	Val					
			385				390						395							
													400							

Phe Tyr Arg Ser Asn Pro Ala Arg Glu Ala Phe Val Glu Met Cys Asn
 405 410 415

Asp Glu Tyr Val Gln Lys Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg
 420 425 430

Val Ala Pro Gly Ser Pro Leu Glu Asp Ile Lys Leu Ala Val Asn Thr
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Ile Gly Ser Leu Val Arg Ala Asn Ala Leu Arg Arg Glu Ile Glu Lys
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Leu Ser Val
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<220>
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32

<210> 10
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 <212> DNA
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<220>
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27

<210> 11
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<220>
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27

<210> 12
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<220>
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<400> 12
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<210> 13
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<212> DNA
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<220>
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<400> 13
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<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 14
ggatcctcca gcggacaagc caac 24

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400>
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<210> 16
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<213> Artificial Sequence

<220>
<223> PCR Primer

<400>
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<210> 17
<211> 32
<212> DNA
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<220>
<223> PCR Primer

<400> 17
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<210> 18
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